

AAGACTACATTAGTTGTGTTGAAARATAAAATGTTAAGTTGTCATTCTTGAACCTCCGACC
 650 660 670 680 690 700 700 710 720

X
GGG
|||
GGG
X

2. US-08-973-363-1 (1-723) 7
 US-08-973-363-15 Sequence 15, Application-US-08973-363 7

Initial Score = 62 Optimized Score = 169 Significance = 0.01
 Residue Identity = 32% Matches = 174 Mismatches = 364
 Gaps = 3 Conservative Substitutions = 0

140 150 160 170 180 X 190 200
 TCTGTAATTATTATTCTTGATCTTGTAGCGGAAGTTGTTGGGATTAGTTAGTTAGTTAGCTGT

210 220 230 240 250 260 270
 TTCTTCCTTGAAACTGACTTTCATTTGCAACATTTGCAAGTGGCTTATTTGCTGTTACAAGTAGTGTGCCA
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 GATCAGAAAGTTATTCTTGAAAGGCAAGAAAGATGGTTAGATCATTTAGTGTACAGTACAGAA
 30 40 50 60 70 80 90

280 290 300 310 320 330 340
 TGGCTGCTTAGAAGTAGTGTAGGAAACATTAGGGAAATACTTGGAGTGGAGCAACAGCTGGTACTGCCAAC
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 TGGACACCACGGAAACTCTACTACATACGGCTACTACGGCTTAAGCTCAACACCTTTAAAGGGAG
 100 110 120 130 140 150 160

350 360 370 380 390 400 410 420
 TGTAGGCTTTGGGATTAGGGGCCACAGAGTTGTGTATAAATTGTTAATGATTTCACTCCGCCCCCTTC
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 AGTTATCAGCAATTGTAAGTTGTTGCTGTTGAGGAACCTTTAAAGACCTGAACTTGAANNGAAAGAGGCC
 170 180 190 200 210 220 230

430 440 450 460 470 480 490
 ATTAAATGCTTGTGTTATGAAACACTCTTTTTTTTTTTGGCTTCTTCATATCCTGTGTTA
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 AGGAGTTGATAGATGAAATCTCGAAAGGNCCTGAAATGAGAATTTGAGTCACTGGCCATTACTGTGAG
 240 250 260 270 280 290 300

510 520 530 540 550 560
 ATGAGTTAATGCTTGAAGCACATGGCAGAACCTGGAGATCTGGTGTGACAGCTGGTACAGGAGCTCTGA
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 GAGATGAGTTACTTCACAGTCAACGTAGTAACCTTCAATATGGTAAAGATGACATTGTA - - - TIGG
 320 330 340 350 360 370

570 580 590 600 610 620 630
 ATTTRTAGATAAACATGAGAGTGGAAACAGAAACTCTGGGTAGTTCTGGCTGACTGTAAATTGTTG
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 AACCAAGAAATCTAAGAACACTGGGAAGAAATCTCAAGAAACTCTGGCTGAGTAGGGNNNG
 380 390 400 410 420 430 440

640 650 660 670 680 690 700
 GAGAAATATTCTCAAGACTACATTAGTTGTTGTTGAGGAAAAAATGTTGAGTTGCTTCCATTCTTGA
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 AAAGGAAATGAAACTTGAGAAATATATGCTTCAGAAATGAGAAACTGTGCTTCAAGAAATGAGATCAGC
 460 470 480 490 500 510 520

710 720 X
 AACCTCCGACCGGG
 ||| |||
 ATGGAAATGAGGGAGATGAGTGGAGAGAAGAATATGTTGATGATGTTGATGTTGATGTTGATGTTG
 530 540 550 560 570 580

	PARAMETERS	K-tuple	Joining	penalty
Similarity matrix	Unitary	1	1	1
Mismatch penalty	1	1	1	1

	Window size
Gap penalty	0.33
Gap size penalty	0.00
Cutoff score	1

KAPUTER 11: LÄRNINGSSÄFÄR 91

Scores:	Mean	Median	Standard deviation
SEARCH STATISTICS	10.00	10.00	0.00

Times: 496 CPO 95 Total Financed 1547.44

Number of residues: 10306
00:00:00.93 00:00:01.00

Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score
---------------	-------------	--------	-------------	------------

ACATAGGACTTACAGAAAGGGGTTCTGACCTACCTGTAACCTGAGCTGAGCTTCTTAACTCTT	150	160	170	180	190-	200	210	
ACATAGGACTTACAGAAAGGGGTTCTGACCTACCTGTAACCTGAGCTGAGCTTCTTAACTCTT	220	220	240	250	260	270	280	
TAATACTACATGAATGGGACAGTGATGAGAAAGTGTAAGAACAGAGTGAGAGTCAGAGTCAG	220	230	240	250	260	270	280	
TAATACTACATGAATGGCAGTGATGAGAAAGTGTAAGAACAGAGTGAGAGTCAGAGTCAG	290	300	310	320	330	340	350	360
ATGAGTATCTGGGTCTAGCTCAGTCAGTTCTGGATCTGGATCTGGAGCTAGTGATGAGATAGCA	290	300	310	320	330	340	350	360
ATGAGTATCTGGGTCTAGCTCAGTCAGTTCTGGATCTGGAGCTAGTGATGAGATAGCA	370	380	390	400	410	420	430	430
GCCAGTCAGTAGCTAGTGTAGCTGAACTCTGGTTCTAGAGTCAGTCAGTCAGTCAGTCAG	370	380	390	400	410	420	430	430
GCCAGTCAGTAGCTAGTGTAGCTGAACTCTGGTTCTAGAGTCAGTCAGTCAGTCAGTCAG	440	450	460	470	480	490	500	500
CTAGAGAGAAAACAGTCAACTCAAACTCTCCAAAAGCTGAGCTGAGCTGAGCTGAGCTGAG	440	450	460	470	480	490	500	500
CTAGAGAGAAAACAGTCAACTCAAACTCTCCAAAAGCTGAGCTGAGCTGAGCTGAGCTGAG	510	520	530	540	550	560	570	570

2240	2250	2260	2270	2280	2290	2300	3170	3180	3190	3200	3210	3220	3230	3240
2310	2320	2330	2340	2350	2360	2370	3170	3180	3190	3200	3210	3220	3230	3240
GAAGACTTAAAGATGTAGAAAGCTTACCTGCTAAGTTGACAAATTCAGGATGCAATGACTG							AAAGGAGGCCAGGAATGGATAATGGATAATGAAATCTGGGAAATGAGCAGGCG							
GAAGACTTAAAGATGTAGAAAGCTTACCTGCTAAGTTGACAAATTCAGGATGCAATGACTG							AAAGGAGGCCAGGAATGGATAATGGATAATGAAATCTGGGAAATGAGCAGGCG							
2310	2320	2330	2340	2350	2360	2370	3170	3180	3190	3200	3210	3220	3230	3240
2380	2390	2400	2410	2420	2430	2440	3250	3260	3270	3280	3290	3300	3310	
CATTGAGAAGAAATTACAACTGGATTAAAGAAATTATAAGGCCCTAGTAAAGGTC							CATTGACTCTAGGGGTGAGTTGCTTACAGTCAAGTGGGAACATTTC							
CATTGAGAAGAAATTACAACTGGATTAAAGAAATTATAAGGCCCTAGTAAAGGTC							CATTGACTCTAGGGGTGAGTTGCTTACAGTCAAGTGGGAACATTTC							
2380	2390	2400	2410	2420	2430	2440	3250	3260	3270	3280	3290	3300	3310	
2450	2460	2470	2480	2490	2500	2510	3250	3260	3270	3280	3290	3300	3310	
GTACCTCAGCCTTCGAGCATATTGAGGAACTTAACTGTTACCTCATTTGCTAACCCATTGCTAACCC							TGAGTGGACCAAGAAATTCAAGGAAATATTCAGTGTGCTTACAGTCAAGGAAAGATG							
GTACCTCAGCCTTCGAGCATATTGAGGAACTTAACTGTTACCTCATTTGCTAACCCATTGCTAACCC							TGAGTGGACCAAGAAATTCAAGGAAATATTCAGTGTGCTTACAGTCAAGGAAAGATG							
2450	2460	2470	2480	2490	2500	2510	3250	3260	3270	3280	3290	3300	3310	
2530	2540	2550	2560	2570	2580	2590	3250	3260	3270	3280	3290	3300	3310	
CAGATGATATGAACTCTATATAAACAGGCTTACAGATTGATCTGATGAGGAACTTAAATCC							AGNGAGGAAGAACAAAGAAACTTGAGAAATAATACATGCTGTCGGAAGAAAGATG							
CAGATGATATGAACTCTATATAAACAGGCTTACAGATTGATCTGATGAGGAACTTAAATCC							AGNGAGGAAGAACAAAGAAACTTGAGAAATAATACATGCTGTCGGAAGAAAGATG							
2530	2540	2550	2560	2570	2580	2590	3250	3260	3270	3280	3290	3300	3310	
2600	2610	2620	2630	2640	2650	2660	3250	3260	3270	3280	3290	3300	3310	
TCTTGACAGCTACGATCTGCTGAGACCTGGGAAACAGGTTCTGATGCTGAGGAGGA							TCACTTGTATGGATGCTGAGGAAACCCCTAGAGAAAGATTCATGCTCCATCA							
TCTTGACAGCTACGATCTGCTGAGACCTGGGAAACAGGTTCTGATGCTGAGGAGGA							TCACTTGTATGGATGCTGAGGAAACCCCTAGAGAAAGATTCATGCTCCATCA							
2600	2610	2620	2630	2640	2650	2660	3250	3260	3270	3280	3290	3300	3310	
2660	2670	2680	2690	2700	2710	2720	3250	3260	3270	3280	3290	3300	3310	
TGCTGGACATCTTACAGGAAATATGTAAAGTATGAACTTGTGCTGAACTTAAAG							CAGAAGAAACGCCAAAGGGTGAAGACCTCTGCAACATTCTGAGAAATTTAGCTG							
TGCTGGACATCTTACAGGAAATATGTAAAGTATGAACTTGTGCTGAACTTAAAG							CAGAAGAAACGCCAAAGGGTGAAGACCTCTGCAACATTCTGAGAAATTTAGCTG							
2660	2670	2680	2690	2700	2710	2720	3250	3260	3270	3280	3290	3300	3310	
2740	2750	2760	2770	2780	2790	2800	3250	3260	3270	3280	3290	3300	3310	
CAAGACCTGGACCTTACGATCATGGATCTGCTGAGACCTGGGAACTGCTGCTA							CTAGACATGCTGAACTCTGGTGTGATTAATCTGAGACGAACTTGGCTGAAATTTGAT							
CAAGACCTGGACCTTACGATCATGGATCTGCTGAGACCTGGGAACTGCTGCTA							CTAGACATGCTGAACTCTGGTGTGATTAATCTGAGACGAACTTGGCTGAAATTTGAT							
2740	2750	2760	2770	2780	2790	2800	3250	3260	3270	3280	3290	3300	3310	
2810	2820	2830	2840	2850	2860	2870	3250	3260	3270	3280	3290	3300	3310	
CAAGACCTGGACCTTACGATCATGGATCTGCTGAGACCTGGGAACTGCTGCTA							CTAGACATGCTGAACTCTGGTGTGATTAATCTGAGACGAACTTGGCTGAAATTTGAT							
CAAGACCTGGACCTTACGATCATGGATCTGCTGAGACCTGGGAACTGCTGCTA							CTAGACATGCTGAACTCTGGTGTGATTAATCTGAGACGAACTTGGCTGAAATTTGAT							
2810	2820	2830	2840	2850	2860	2870	3250	3260	3270	3280	3290	3300	3310	
2890	2900	2910	2920	2930	2940	2950	3250	3260	3270	3280	3290	3300	3310	
CAACAGATATGCGAGGCAAGCGAGCTCATAGGAACTGAGGAAACAGCTTACGTTACGCTG							CTGATAGGGTTAACGACATTCATCTGGGAACTTGGCTGAGCTTGGAGTAAAGGCC							
CAACAGATATGCGAGGCAAGCGAGCTCATAGGAACTGAGGAAACAGCTTACGTTACGCTG							CTGATAGGGTTAACGACATTCATCTGGGAACTTGGCTGAGCTTGGAGTAAAGGCC							
2890	2900	2910	2920	2930	2940	2950	3250	3260	3270	3280	3290	3300	3310	
2960	2970	2980	2990	3000	3010	3020	3250	3260	3270	3280	3290	3300	3310	
TAGTCACAAAGGATCTAGTAAAGCAATTTCTGAAAGGCCAGAGAACTGCTGCTA							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
TAGTCACAAAGGATCTAGTAAAGCAATTTCTGAAAGGCCAGAGAACTGCTGCTA							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
2960	2970	2980	2990	3000	3010	3020	3250	3260	3270	3280	3290	3300	3310	
3030	3040	3050	3060	3070	3080	3090	3250	3260	3270	3280	3290	3300	3310	
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
3030	3040	3050	3060	3070	3080	3090	3250	3260	3270	3280	3290	3300	3310	
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
3100	3110	3120	3130	3140	3150	3160	3250	3260	3270	3280	3290	3300	3310	
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
TAATTCAGAGATGGACACACAGAAACTGTCCTGATCACGTTACGCTGAACTGCTG							CAACCTTCGAACTCTCAGGACTGAGCTGAACTTGGCTGAGCTTGGAGTAAAGGCC							
3100	3110	3120	3130	3140	3150	3160	3250	3260	3270	3280	3290	3300	3310	

1. US-08-973-363-10 (1-6608)
 US-08-973-363-3 Sequence 3, Application US/08973363
 Initial Score = 103 Optimized Score = 115 Significance = -0.25
 Residue Identity = 75% Matches = 115 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

2. US-08-973-363-10 (1-6608)
 US-08-973-363-3 Sequence 3, Application US/08973363
 Initial Score = 103 Optimized Score = 115 Significance = -0.25
 Residue Identity = 75% Matches = 115 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

3. US-08-973-363-10 (1-6608)
 US-08-973-363-32 Sequence 32, Application US/08973363
 Initial Score = 111 Optimized Score = 111 Significance = -0.25
 Residue Identity = 100% Matches = 111 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

4. US-08-973-363-10 (1-6608)
 US-08-973-363-34 Sequence 34, Application US/08973363
 Initial Score = 101 Optimized Score = 101 Significance = -0.26
 Residue Identity = 90% Matches = 101 Mismatches = 10
 Gaps = 0 Conservative Substitutions = 0

5. US-08-973-363-10 (1-6608)
 US-08-973-363-34 Sequence 34, Application US/08973363
 Initial Score = 101 Optimized Score = 101 Significance = -0.26
 Residue Identity = 90% Matches = 101 Mismatches = 10
 Gaps = 0 Conservative Substitutions = 0

6. US-08-973-363-10 (1-6608)
 US-08-973-363-36 Sequence 36, Application US/08973363
 Initial Score = 99 Optimized Score = 99 Significance = -0.26
 Residue Identity = 89% Matches = 99 Mismatches = 12
 Gaps = 0 Conservative Substitutions = 0

3520 ACTCCATCACAGAAAGAAAACGGCCAAAAGGGGGAGACCTCGAACCCATTCTCGAAAGATATTCGGTGTGAACTATTCGGTGTGAACTAACAG
 3450 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 GGCCTGGCTGGCAGGCAATTCCAGAGACTACTATTAATTAATGAAAGACCCAGGAAATAAGGAGCTTATCAGAGTTACAAGAAATTGGTGGCCCTCTGGAAAG
 3420 4210 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250
 AGCAGGTTACAGACCCGGTGGAGACTACTATTAATTAATGAAAGACCCAGGAAATAAGGAGCTTATCAGAGTTACAAGAAATTGGTGGCCCTCTGGAAAG
 3350 3450 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 GATTTAGTCATGCAGAGATCAGGGGTTTATCAGAGTTACAAGAAATTGGTGGCCCTCTGGAAAG
 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 CAAACAGATCAGCTTAATGGGAGTGGAGGAGACCGAGTAGGGAGAAGATAATTGGGAGTGGAGGAGACCGAGTAGGGAGAAGATAATTGGGAGTGGAG
 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 ACTCCATCACAGAAAGAAAACGGCCAAAAGGGGGAGACCTCGAACCCATTCTCGAAAGATATTCGGTGTGAACTATTCGGTGTGAACTAACAG
 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 GATTTAGTCATGCAGAGATCAGGGGTTTATCAGAGTTACAAGAAATTGGTGGCCCTCTGGAAAG
 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650
 AGAAAGAAACGGCCAAAAGGGGGTTATCAGAGTTACAAGAAATTGGTGGCCCTCTGGAAAG

3450	3460	3470	3480	3490	3500	3510
CAAAACAGATCAGCTTAAATGGGAGTGAAGGAAGCAGCTAGGAGCAGATTCGGATCTGATCTGATCTG						
X	10	20				
3520	3530	3540	3550	3560	3570	3580
ACTCCATACAGAAAGAAACGCCAAAARGCGTGGAAAGACCTCCAAACATTCTCGAGAAAATTTAAAG						
X	10	20				
ATTCAACATCAGAAAGGAAACGCCGAAAGACCTCCAAACATTCTCGAGAAAATTTAAAG						
X	10	20				
3600	X	3620	3630	3640	3650	
GATTAGTAGAGCAAGATCAGCGGGTTATCAAGAGTTACAGAAAATTGGGGCCCTCTGGAAAG						
X	10	20				
GATTAGTAGATGCGAG						
X	10	20				
2. US-08-973-363-10 (1-6608)						
US-08-973-363-33 Sequence 33, Application US/08973363						
Initial Score = 61 Optimized Score = 61 Significance = -0.28						
Residue Identity = 91% Matches = 61 Mismatches = 6						
Alps = 0 Conservative Substitutions = 0						
3480	3490	3500	3510	3520	3530	3540
AGTGAAGGAAACGAGCTAGGAGCAGAGTAACTGGATCTGATCTGGATCTGATCTGGATCTGATCTG						
X	10	20				
3550	3560	3570	3580	3590	3600	3610
CCAAAAGGCGGGAGAACCTCCAAACATTCTCGAGAAAATTTAAAGGATTAGTGTAGAGATCAGG						
X	10	20				
CCAAAAGGCTGGAGAACCCACGAACTTCTCGAGAAAATTTAAAGGATTAGTGTAGAGATCAGG						
X	10	20				
3620	3630	3640	3650	3660	3670	3680
CGGTTTATCAAGAGTTACAGAAA						
X	10	20				
3. US-08-973-363-10 (1-6608)						
US-08-973-363-35 Sequence 35, Application US/08973363						
Initial Score = 59 Optimized Score = 59 Significance = -0.28						
Residue Identity = 88% Matches = 59 Mismatches = 6						
Alps = 0 Conservative Substitutions = 0						
3480	3490	3500	3510	3520	3530	3540
AGTGAAGGAAACGCGAGTGGAGCAGAGTAACTGGATCTGATCTGGATCTGATCTGGATCTGATCTG						
X	10	20				
3550	3560	3570	3580	3590	3600	3610
CCAAAAGGCGGGAGAACCTCCAAACATTCTCGAGAAAATTTAAAGGATTAGTGTAGAGATCAGG						
X	10	20				
CCAAAAGGACCTGGAGCACGAACTTCTCGAGAAAATTTAAAGGATTAGTGTAGAGATCAGG						
X	10	20				
3620	3630	3640	3650	3660	3670	3680
CGGTTTATCAAGAGTTACAGAAA						
X	10	20				
4. US-08-973-363-10 (1-6608)						
US-08-973-363-1 Sequence 1, Application US/08973363						
Initial Score = 49 Optimized Score = 252 Significance = -0.29						
Residue Identity = 38% Matches = 290 Mismatches = 433						
Alps = 32 Conservative Substitutions = 0						

4. US-08-978-363-10 (1-5609) Sequence 1, Application US/097336
US-08-978-363-1

1. US-08-973-363-10 (1-6608) US-08-973-363-2 Sequence 1, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Residue Identity = 628 Matches = 60 Conservative Substitutions = 96 Mismatches = - 57 Gaps = 0
2. US-08-973-363-3 Sequence 2, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 94 Mismatches = - 17 Gaps = 0	Initial Score = 91 Optimized Score = 91 Matches = 84% Conservative Substitutions = 94 Mismatches = - 0
3. US-08-973-363-4 Sequence 4, Application US/08973363	Initial Score = 98 Optimized Score = 111 Significance = -0.26 Residue Identity = 73% Matches = 119 Conservative Substitutions = 34 Gaps = 9	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 1
4. US-08-973-363-5 Sequence 5, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
5. US-08-973-363-6 Sequence 6, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
6. US-08-973-363-7 Sequence 7, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
7. US-08-973-363-10 (1-6608) US-08-973-363-4 Sequence 4, Application US/08973363	Initial Score = 98 Optimized Score = 111 Significance = -0.26 Residue Identity = 73% Matches = 119 Conservative Substitutions = 34 Gaps = 9	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
8. US-08-973-363-10 (1-6608) US-08-973-363-5 Sequence 5, Application US/08973363	Initial Score = 94 Optimized Score = 107 Significance = -0.26 Residue Identity = 69% Matches = 107 Conservative Substitutions = 0 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
9. US-08-973-363-10 (1-6608) US-08-973-363-2 Sequence 2, Application US/08973363	Initial Score = 94 Optimized Score = 96 Significance = -0.26 Residue Identity = 84% Matches = 94 Conservative Substitutions = 94 Mismatches = - 0	Initial Score = 91 Optimized Score = 91 Matches = 84% Conservative Substitutions = 94 Mismatches = - 0
10. US-08-973-363-10 (1-6608) US-08-973-363-12 Sequence 12, Application US/08973363	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0	Initial Score = 94 Optimized Score = 115 Significance = -0.26 Residue Identity = 45% Matches = 120 Conservative Substitutions = 120 Mismatches = - 144 Gaps = 0
11. US-08-973-363-10 (1-6608) US-08-973-363-31 Sequence 31, Application US/08973363	Initial Score = 91 Optimized Score = 91 Matches = 84% Conservative Substitutions = 94 Mismatches = - 0	Initial Score = 91 Optimized Score = 94 Matches = 94 Conservative Substitutions = 94 Mismatches = - 0

PARAMETERS

Similarity matrix	Unitary	K-tuple joining penalty	4
Mismatch penalty	1	30	
GAP penalty	5.00	500	
Gap size penalty	0.33		
Cutoff score	1		
Randomization group	0		

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SEARCH STATISTICS

Scoring: Mean Median Standard Deviation

32	27	22.27
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Times: CPU Total Elapsed

00:00:00.00
00:00:01.00

Number of records: 10206

Number of sequences : 10300
Number of issues : 18

Number of scores above cutoff: 18

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

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The list of best scores is:

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

TTTCAAGACTACATTAGTGTGTTGGAAA--ATAAAATGTTAAGTGTCCATTCTTGAACCT	650	660	670	680	690	700	710
TCGACCGGG							
TCGGACCGGG							
720 X							
US-08-973-163-1' (1-723)							
US-08 973-363-10 Sequence 10, Application US/089733363							
Initial Score = 80 Optimized Score = 257 Significance = 2.16							
Residue Identity = 38% Matches = 277 Mismatches = 442							
Alaps = 8 Conservative Substitutions = 0							
ATCATCAGGGAGGGAGGAGCGATGATGAAGAATTATGATAAGAGGATCTCGCCAGGAAACATGTA	870	880	890	900	910	920	930
ATGGCAACTTAACATTATTTCTCAAACACAACTAATGAGTCCTGTTCAACT	940	950	960	970	980	990	1000
ATGTTAGTTACAAGAACAGCTGAAGAACCAAGACAGA-TTCTGTGATTGCTGAAAGTTGTGGAGGAGAT	1010	1020	1030	1040	1050	1060	1070
TTACAGTCAGCTCAGAACACTAGCCTCAGATTCTCTAGTTCTGTTCCACT	1080	1090	1100	1110	1120	1130	1140
GCCCCACAGACTGAAGAACAGTGAATTTGAAACTATAGAGAAAGTTATGGCACATGGCAATGGCGAAAAGGAA	1150	1160	1170	1180	1190	1200	1210
GCTCTGTGACCTGCTCATCACAGATCTCTAGTTCTGCATGTTCTAACTCATTACCA	1220	1230	1240	1250	1260	1270	1280
GGAGGATGAGAACCCAAAAAAAGGGAGGTTCTAAACAGGAAATTAAATGGAAAG	1310	1320	1330	1340	1350	1360	1370
GCAGGGCAGGATATCATTAACAAATTATACAACTCTGTTCTCAAACTCCAAATCAGCTTGTGGCTTCCTCAATTCAGCTTGT	1440	1450	1460	1470	1480	1490	1500
ACTGAGAACCGCTGAAGCAAAATGTTAAAGGAAATGACAAACTGCAACTACAAAGGATCAG	1560	1570	1580	1590	1600	1610	1620



Results file seq01inv-land15.res made by mruhl

Query sequence being compared: US-08-973-363-10

Number of sequences searched: 10

Number of scores above cutoff: 5

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results of the initial comparison of US-08-973-363-10

File : US08973363.seq

Score	0	10	50	100
0	0	0	0	0
10	0	0	0	0
50	0	0	0	0
100	0	0	0	0
200	0	0	0	0
300	0	0	0	0
400	0	0	0	0
500	0	0	0	0
600	0	0	0	0
700	0	0	0	0
800	0	0	0	0
900	0	0	0	0
1000	0	0	0	0
1100	0	0	0	0
1200	0	0	0	0
1300	0	0	0	0
1400	0	0	0	0
1500	0	0	0	0
1600	0	0	0	0
1700	0	0	0	0
1800	0	0	0	0
1900	0	0	0	0
2000	0	0	0	0
2100	0	0	0	0
2200	0	0	0	0
2300	0	0	0	0
2400	0	0	0	0
2500	0	0	0	0
2600	0	0	0	0
2700	0	0	0	0
2800	0	0	0	0
2900	0	0	0	0
3000	0	0	0	0
3100	0	0	0	0
3200	0	0	0	0
3300	0	0	0	0
3400	0	0	0	0
3500	0	0	0	0
3600	0	0	0	0
3700	0	0	0	0
3800	0	0	0	0
3900	0	0	0	0
4000	0	0	0	0
4100	0	0	0	0
4200	0	0	0	0
4300	0	0	0	0
4400	0	0	0	0
4500	0	0	0	0
4600	0	0	0	0
4700	0	0	0	0
4800	0	0	0	0
4900	0	0	0	0
5000	0	0	0	0
5100	0	0	0	0
5200	0	0	0	0
5300	0	0	0	0
5400	0	0	0	0
5500	0	0	0	0
5600	0	0	0	0
5700	0	0	0	0
5800	0	0	0	0
5900	0	0	0	0
6000	0	0	0	0
6100	0	0	0	0
6200	0	0	0	0
6300	0	0	0	0
6400	0	0	0	0
6500	0	0	0	0
6600	0	0	0	0
6700	0	0	0	0
6800	0	0	0	0
6900	0	0	0	0
7000	0	0	0	0
7100	0	0	0	0
7200	0	0	0	0
7300	0	0	0	0
7400	0	0	0	0
7500	0	0	0	0
7600	0	0	0	0
7700	0	0	0	0
7800	0	0	0	0
7900	0	0	0	0
8000	0	0	0	0
8100	0	0	0	0
8200	0	0	0	0
8300	0	0	0	0
8400	0	0	0	0
8500	0	0	0	0
8600	0	0	0	0
8700	0	0	0	0
8800	0	0	0	0
8900	0	0	0	0
9000	0	0	0	0
9100	0	0	0	0
9200	0	0	0	0
9300	0	0	0	0
9400	0	0	0	0
9500	0	0	0	0
9600	0	0	0	0
9700	0	0	0	0
9800	0	0	0	0
9900	0	0	0	0
10000	0	0	0	0

PARAMETERS

Similarity matrix	Unitary	K-tuple
Mismatch penalty	1	Joining penalty
Gap penalty	5.00	Window size
Gap size penalty	0.33	
Cutoff score	1	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median
Times:	32	24
CPU	00:00:00.03	
Number of residues:	1036	
Number of sequences searched:	18	
Number of scores above cutoff:	18	

The scores below are sorted by initial score. Significance is calculated based on initial score. A 100% identical sequence to the query sequence is:

US-08-973-363-10' (1-6608) US-08-973-363-12 Sequence 12, Application US/08973363	Initial Score = 40 Optimized Score = 102 Significance = 0.32 Residue Identity = 41% Matches = 120 Mismatches = 145 Gaps = 26 Conservative Substitutions = 0	31 Optimized Score = 49 Significance = 0.92 Residue Identity = 35% Matches = 55 Mismatches = 0 Gaps = 6 Conservative Substitutions
	70 TAACATTCGTTAATTAAGTCATTCAAATCTCTAAATTAACCTGCTGCAATTGACATTATT 150 GCCCATGTTAAAGGGAAAACAAATGGATTACATGATGATCTGGCTGAGTTGAGTGTACCC 210 ATCTACATAAAAAAATAAAAACAGAAAAAAATGAGAAAAGCCCTAGGCCAGATATTG-----GTA 270 TATAGAAACTTCCCTCTTTAACACAATGACCCGACAGCTTACAGTGTGGATATT 330 TAAAGAAGGAAGCTGGAGAAAAAGAGAGACAAAAGAGAAGGAAATGAAAAGGG----- 390 110 110 120 130 140 150	2970 2980 2990 3000 3010 3020 3030 CAAATTCCTGTTGAAACGCCCTGATCTCTGCACTAAATCTTAAATTTCTGAG ATTTCCTGATGATCCAGAGX 10 20
	3040 3050 3060 3070 3080 3090 3100 GAGAAACCCCGCCAAAGCAGGTACAGACCAAGAAACCCAGGCCAAACAGCTACAGGCCGAGACTA 360 40 50 60 70 80 90	3040 3050 3060 3070 3080 3090 3100 TGTTTCCAGGCTTCCACGCTTTCGGTTTTCCTGTATGGAGTCACTATGAGTCAGAACTGAG 320 40 50 60 70 80 90
	110 110 120 130 140 150 X	110 110 120 130 140 150 X
	3120 3130 3140 3150 3160 X 3170 TCCTCTCTTCACTCCCTAAATGAGTCATGTTGGACAGTTCTCAT 380 40 50 60 70 80 90	3120 3130 3140 3150 3160 X 3170 TCATTAATTAATCTGAAATAAGCTCTTCAAGAAGGAGGACAAAGGCTTGGCTGTTGCA 440 50 60 70 80 90
	110 110 120 130 140 150 X	110 110 120 130 140 150 X
	3180 3190 3200 3210 TCGGGAGCATGATATACTCTCAAGTCTTGTCT	3180 3190 3200 3210 TCGGGAGCATGATATACTCTCAAGTCTTGTCT
	440 50 60 70 80 90	440 50 60 70 80 90
8. US-08-973-363-10' (1-6608) US-08-973-363-4 Sequence 4, Application US/08973363	Initial Score = 30 Optimized Score = 56 Significance = -0.08 Residue Identity = 36% Matches = 56 Mismatches = 0 Gaps = 0 Conservative Substitutions.	5770 5780 5790 5800 5810 5820 5830 TGTGCTCTTTCCTCCACTTTGGCTTAATCTGCTGGAGGGTTAGGCTTTGACTTGTGTTTGGC 640 700 800 900 1000 1100 1200 1300 1400 1500 X
	30 40 50 60 70 80 90	30 40 50 60 70 80 90
	5850 5860 5870 5880 5890 5900 5910 ATAGTCAGATTCACCTTCTTACAACCTGCTTTATCCCCATCTTCCGGATTGAGTCAGACCACTT 640 700 800 900 1000 1100 1200 1300 1400 1500 X	5850 5860 5870 5880 5890 5900 5910 AGAAACCCAGGCTTAAGCAGTTACAGACCCAGAAACCCAGGCTTAACAGCTTACAGACCTGAGATTAA 640 700 800 900 1000 1100 1200 1300 1400 1500 X
	30 40 50 60 70 80 90	30 40 50 60 70 80 90
	5920 5930 5940 5950 5960 5970 X 5980 TGATATGACCCCTGACCTGACATTGCCAGTCTCTCATCTTATGCTTTCTCTCTAGTTAACCTGAC 700 750 800 850 900 950 1000 1100 1200 1300 1400 1500 X	5920 5930 5940 5950 5960 5970 X 5980 TCATTAATTAATCTGAAATAAGACCTGCAASAAAGGAGACACTTGGTGGTGC 700 750 800 850 900 950 1000 1100 1200 1300 1400 1500 X
	30 40 50 60 70 80 90	30 40 50 60 70 80 90
	5990 6000 6010 6020 ATCATGGGAGAAATCTCACTACTGATGATCTCT	5990 6000 6010 6020 ATCATGGGAGAAATCTCACTACTGATGATCTCT
	3720 3730 3740 3750 3760 3770 3780 CTCTGCAAGTCATCTGTTGATTCCTGAGTCAAGAACTACAATGAGTCAGGATGCAAGTTAAC 430 440 450 460 470 480 490	3720 3730 3740 3750 3760 3770 3780 AAAACCAAGAAAACAGTTACAGACCCAAACAGAAACAGTTA-CAGACCCGTCAGACTAC 400 410 420 430 440 450 460
	3790 3800 3810 3820 3830 3840 X 3850 CTAATCCCTCCAGCTCTGTTGAGCTAAACAGAAATCTGATCTCTGCAATGAAATGATCCAGTG 460 470 480 490 500 510 520 530 540 550 560	3790 3800 3810 3820 3830 3840 X 3850 CTCATCAACACTAGAGAGATCTGCAAGAGCTTGTGGTGGCG 460 470 480 490 500 510 520 530 540 550 560
	3860 3870 3880 3890 CTTGCTTCCTCATTCCTTTATGATCCATCAAGT	3860 3870 3880 3890 CTTGCTTCCTCATTCCTTTATGATCCATCAAGT

